

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Larsen, Glenn
Sako, Dianne
Chang, Xiao Jia
Veldman, Geertruida M.
Cumming, Dale
Kumar, Ravindra
Shaw, Gray
- (ii) TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LEGAL AFFAIRS
 - (B) STREET: 87 CAMBRIDGE PARK DRIVE
 - (C) CITY: CAMBRIDGE
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/965,662
 - (B) FILING DATE: 23-OCT-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/112,608
 - (B) FILING DATE: 26-AUG-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/10168
 - (B) FILING DATE: 22-OCT-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/235,398
 - (B) FILING DATE: 28-APR-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/316,305
 - (B) FILING DATE: 30-SEP-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/428,734
 - (B) FILING DATE: 25-APR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWN, SCOTT A.
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: GI 5213F
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (G) CELL TYPE: Promyelocyte
 (H) CELL LINE: HL60

(vii) IMMEDIATE SOURCE:
 (B) CLONE: PMT21:PL85

(ix) FEATURE:
 (A) NAME/KEY: 5'UTR
 (B) LOCATION: 1..59

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 60..1268

(ix) FEATURE:
 (A) NAME/KEY: 3'UTR
 (B) LOCATION: 1269..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GCCACTTCTT CTGGGCCAC GAGGCAGCTG TCCCATGCTC TGCTGAGCAC GGTGGTGCC      59
ATG CCT CTG CAA CTC CTC CTG TTG CTG ATC CTA CTG GGC CCT GGC AAC      107
Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
  1             5             10             15
AGC TTG CAG CTG TGG GAC ACC TGG GCA GAT GAA GCC GAG AAA GCC TTG      155
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
          20          25          30
GGT CCC CTG CTT GCC CGG GAC CGG AGA CAG GCC ACC GAA TAT GAG TAC      203
Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
          35          40          45
CTA GAT TAT GAT TTC CTG CCA GAA ACG GAG CCT CCA GAA ATG CTG AGG      251
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
          50          55          60
AAC AGC ACT GAC ACC ACT CCT CTG ACT GGG CCT GGA ACC CCT GAG TCT      299
Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
          65          70          75          80
ACC ACT GTG GAG CCT GCT GCA AGG CGT TCT ACT GGC CTG GAT GCA GGA      347
Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
          85          90          95
GGG GCA GTC ACA GAG CTG ACC ACG GAG CTG GCC AAC ATG GGG AAC CTG      395
Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
          100          105          110
TCC ACG GAT TCA GCA GCT ATG GAG ATA CAG ACC ACT CAA CCA GCA GCC      443
Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
          115          120          125
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ACG Thr	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro	CTG Leu	GCA Ala	GCC Ala	ACA Thr	GAG Glu	GCA Ala	CAG Gln	ACA Thr	ACT Thr	491
130						135					140					
CGA Arg	CTG Leu	ACG Thr	GCC Ala	ACG Thr	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro	CTG Leu	GCA Ala	GCC Ala	ACA Thr	GAG Glu	539
145					150					155					160	
GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro	CCA Pro	GCA Ala	GCC Ala	ACG Thr	GAA Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CAA Gln	CCC Pro	587
				165					170					175		
ACA Thr	GGC Gly	CTG Leu	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	GCA Ala	CCA Pro	GCA Ala	GCC Ala	ATG Met	GAG Glu	GCA Ala	CAG Gln	635
			180					185					190			
ACC Thr	ACT Thr	GCA Ala	CCA Pro	GCA Ala	GCC Ala	ATG Met	GAA Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro	CCA Pro	GCA Ala	GCC Ala	583
		195					200					205				
ATG Met	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CAA Gln	ACC Thr	ACA Thr	GCC Ala	ATG Met	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	731
	210					215					220					
GCA Ala	CCA Pro	GAA Glu	GCC Ala	ACG Thr	GAG Glu	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CAA Gln	CCC Pro	ACA Thr	GCC Ala	ACG Thr	GAG Glu	779
225					230					235					240	
GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro	CTG Leu	GCA Ala	GCC Ala	ATG Met	GAG Glu	GCC Ala	CTG Leu	TCC Ser	ACA Thr	GAA Glu	CCC Pro	827
				245					250					255		
AGT Ser	GCC Ala	ACA Thr	GAG Glu	GCC Ala	CTG Leu	TCC Ser	ATG Met	GAA Glu	CCT Pro	ACT Thr	ACC Thr	AAA Lys	AGA Arg	GGT Gly	CTG Leu	875
			260					265					270			
TTC Phe	ATA Ile	CCC Pro	TTT Phe	TCT Ser	GTG Val	TCC Ser	TCT Ser	GTT Val	ACT Thr	CAC His	AAG Lys	GGC Gly	ATT Ile	CCC Pro	ATG Met	923
		275					280					285				
GCA Ala	GCC Ala	AGC Ser	AAT Asn	TTG Leu	TCC Ser	GTC Val	AAC Asn	TAC Tyr	CCA Pro	GTG Val	GGG Gly	GCC Ala	CCA Pro	GAC Asp	CAC His	971
	290					295					300					
ATC Ile	TCT Ser	GTG Val	AAG Lys	CAG Gln	TGC Cys	CTG Leu	CTG Leu	GCC Ala	ATC Ile	CTA Leu	ATC Ile	TTG Leu	GCG Ala	CTG Leu	GTG Val	1019
305					310					315					320	
GCC Ala	ACT Thr	ATC Ile	TTC Phe	TTC Phe	GTG Val	TGC Cys	ACT Thr	GTG Val	GTG Val	CTG Leu	GCG Ala	GTC Val	CGC Arg	CTC Leu	TCC Ser	1067
				325					330					335		
CGC Arg	AAG Lys	GGC Gly	CAC His	ATG Met	TAC Tyr	CCC Pro	GTG Val	CGT Arg	AAT Asn	TAC Tyr	TCC Ser	CCC Pro	ACC Thr	GAG Glu	ATG Met	1115
			340					345					350			
GTC Val	TGC Cys	ATC Ile	TCA Ser	TCC Ser	CTG Leu	TTG Leu	CCT Pro	GAT Asp	GGG Gly	GGT Gly	GAG Glu	GGG Gly	CCC Pro	TCT Ser	GCC Ala	1163
		355					360					365				
ACA Thr	GCC Ala	AAT Asn	GGG Gly	GGC Gly	CTG Leu	TCC Ser	AAG Lys	GCC Ala	AAG Lys	AGC Ser	CCG Pro	GGC Gly	CTG Leu	ACG Thr	CCA Pro	1211
	370					375					380					
GAG Glu	CCC Pro	AGG Arg	GAG Glu	GAC Asp	CGT Arg	GAG Glu	GGG Gly	GAT Asp	GAC Asp	CTC Leu	ACC Thr	CTG Leu	CAC His	AGC Ser	TTC Phe	1259
385					390					395					400	

CTC CCT TAGCTCACTC TGCCATCTGT TTTGGCAAGA CCCCACCTCC ACGGGCTCTC . 1315
Leu Pro

CTGGGCCACC CCTGAGTGCC CAGACCCCAA TCCACAGCTC TGGGCTTCCT CGGAGACCCC 1375
TGGGGATGGG GATCTTCAGG GAAGGAATC TGGCCACCCA AACAGGACAA GAGCAGCCTG 1435
GGGCCAAGCA GACGGGCAAG TGGAGCCACC TCTTCTCTCC CTCCGCGGAT GAAGCCCAGC 1495
CACATTTTCAG CCGAGGTCCA AGGCAGGAGG CCATTTACTT GAGACAGATT CTCTCCTTTT 1555
TCCTGTCCCC CATCTTCTCT GGGTCCCTCT AACATCTCCC ATGGCTCTCC CCGCTTCTCC 1615
TGGTCACTGG AGTCTCCTCC CCATGTACCC AAGG 1649

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Leu	Gln	Leu	Leu	Leu	Leu	Ile	Leu	Leu	Gly	Pro	Gly	Asn	
1				5				10					15		
Ser	Leu	Gln	Leu	Trp	Asp	Thr	Trp	Ala	Asp	Glu	Ala	Glu	Lys	Ala	Leu
			20					25					30		
Gly	Pro	Leu	Leu	Ala	Arg	Asp	Arg	Arg	Gln	Ala	Thr	Glu	Tyr	Glu	Tyr
			35				40					45			
Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro	Glu	Met	Leu	Arg
	50					55					60				
Asn	Ser	Thr	Asp	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gly	Thr	Pro	Glu	Ser
	65				70					75					80
Thr	Thr	Val	Glu	Pro	Ala	Ala	Arg	Arg	Ser	Thr	Gly	Leu	Asp	Ala	Gly
				85					90					95	
Gly	Ala	Val	Thr	Glu	Leu	Thr	Thr	Glu	Leu	Ala	Asn	Met	Gly	Asn	Leu
			100					105					110		
Ser	Thr	Asp	Ser	Ala	Ala	Met	Glu	Ile	Gln	Thr	Thr	Gln	Pro	Ala	Ala
		115				120						125			
Thr	Glu	Ala	Gln	Thr	Thr	Pro	Leu	Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr
	130					135					140				
Arg	Leu	Thr	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Pro	Leu	Ala	Ala	Thr	Glu
	145				150					155					160
Ala	Gln	Thr	Thr	Pro	Pro	Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Gln	Pro
				165					170					175	
Thr	Gly	Leu	Glu	Ala	Gln	Thr	Thr	Ala	Pro	Ala	Ala	Met	Glu	Ala	Gln
			180					185					190		
Thr	Thr	Ala	Pro	Ala	Ala	Met	Glu	Ala	Gln	Thr	Thr	Pro	Pro	Ala	Ala
			195				200					205			

Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr Thr
210 215 220

Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu
225 230 235 240

Ala Gln Thr Thr Pro Leu Ala Ala Met Glu Ala Leu Ser Thr Glu Pro
245 250 255

Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
260 265 270

Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
275 280 285

Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
290 295 300

Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
305 310 315 320

Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
325 330 335

Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
340 345 350

Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
355 360 365

Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
370 375 380

Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
385 390 395 400

Leu Pro

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (G) CELL TYPE: placenta

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CCT CTG CAA CTC CTC CTG TTG CTG ATC CTA CTG GGC CCT GGC AAC	48
Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn	
1 5 10 15	
AGC TTG CAG CTG TGG GAC ACC TGG GCA GAT GAA GCC GAG AAA GCC TTG	96
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu	

20					25					30						
GGT Gly	CCC Pro	CTG Leu 35	CTT Leu	GCC Ala	CGG Arg	GAC Asp	CGG Arg 40	AGA Arg	CAG Gln	GCC Ala	ACC Thr	GAA Glu 45	TAT Tyr	GAG Glu	TAC Tyr	144
CTA Leu	GAT Asp 50	TAT Tyr	GAT Asp	TTC Phe	CTG Leu	CCA Pro 55	GAA Glu	ACG Thr	GAG Glu	CCT Pro	CCA Pro 60	GAA Glu	ATG Met	CTG Leu	AGG Arg	192
AAC Asn 65	AGC Ser	ACT Thr	GAC Asp	ACC Thr	ACT Thr 70	CCT Pro	CTG Leu	ACT Thr	GGG Gly	CCT Pro 75	GGA Gly	ACC Thr	CCT Pro	GAG Glu	TCT Ser 80	240
ACC Thr	ACT Thr	GTG Val	GAG Glu	CCT Pro 85	GCT Ala	GCA Ala	AGG Arg	CGT Arg	TCT Ser 90	ACT Thr	GGC Gly	CTG Leu	GAT Asp	GCA Ala 95	GGA Gly	288
GGG Gly	GCA Ala	GTC Val	ACA Thr 100	GAG Glu	CTG Leu	ACC Thr	ACG Thr 105	GAG Glu	CTG Leu	GCC Ala	AAC Asn	ATG Met	GGG Gly 110	AAC Asn	CTG Leu	336
TCC Ser	ACG Thr	GAT Asp 115	TCA Ser	GCA Ala	GCT Ala	ATG Met	GAG Glu 120	ATA Ile	CAG Gln	ACC Thr	ACT Thr	CAA Gln 125	CCA Pro	GCA Ala	GCC Ala	384
ACG Thr	GAG Glu 130	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CAA Gln 135	CCA Pro	GTG Val	CCC Pro	ACG Thr	GAG Glu 140	GCA Ala	CAG Gln	ACC Thr	ACT Thr	432
CCA Pro 145	CTG Leu	GCA Ala	GCC Ala	ACA Thr	GAG Glu 150	GCA Ala	CAG Gln	ACA Thr	ACT Thr	CGA Arg 155	CTG Leu	ACG Thr	GCC Ala	ACG Thr	GAG Glu 160	480
GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro 165	CTG Leu	GCA Ala	GCC Ala	ACA Thr	GAG Glu 170	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro 175	CCA Pro	528
GCA Ala	GCC Ala	ACG Thr	GAA Glu 180	GCA Ala	CAG Gln	ACC Thr	ACT Thr 185	CAA Gln	CCC Pro	ACA Thr	GGC Gly	CTG Leu 190	GAG Glu	GCA Ala	CAG Gln	576
ACC Thr	ACT Thr	GCA Ala 195	CCA Pro	GCA Ala	GCC Ala	ATG Met	GAG Glu 200	GCA Ala	CAG Gln	ACC Thr	ACT Thr	GCA Ala 205	CCA Pro	GCA Ala	GCC Ala	624
ATG Met	GAA Glu 210	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro 215	CCA Pro	GCA Ala	GCC Ala	ATG Met	GAG Glu 220	GCA Ala	CAG Gln	ACC Thr	ACT Thr	672
CAA Gln 225	ACC Thr	ACA Thr	GCC Ala	ATG Met	GAG Glu 230	GCA Ala	CAG Gln	ACC Thr	ACT Thr	GCA Ala 235	CCA Pro	GAA Glu	GCC Ala	ACG Thr	GAG Glu 240	720
GCA Ala	CAG Gln	ACC Thr	ACT Thr	CAA Gln 245	CCC Pro	ACA Thr	GCC Ala	ACG Thr	GAG Glu 250	GCA Ala	CAG Gln	ACC Thr	ACT Thr	CCA Pro 255	CTG Leu	768
GCA Ala	GCC Ala	ATG Met	GAG Glu 260	GCC Ala	CTG Leu	TCC Ser	ACA Thr	GAA Glu 265	CCC Pro	AGT Ser	GCC Ala	ACA Thr	GAG Glu 270	GCC Ala	CTG Leu	816
TCC Ser	ATG Met	GAA Glu 275	CCT Pro	ACT Thr	ACC Thr	AAA Lys	AGA Arg 280	GGT Gly	CTG Leu	TTC Phe	ATA Ile	CCC Pro 285	TTT Phe	TCT Ser	GTG Val	864
TCC	TCT	GTT	ACT	CAC	AAG	GGC	ATT	CCC	ATG	GCA	GCC	AGC	AAT	TTG	TCC	912

Ser	Ser	Val	Thr	His	Lys	Gly	Ile	Pro	Met	Ala	Ala	Ser	Asn	Leu	Ser	
290						295					300					
GTC	AAC	TAC	CCA	GTG	GGG	GCC	CCA	GAC	CAC	ATC	TCT	GTG	AAG	CAG	TGC	960
Val	Asn	Tyr	Pro	Val	Gly	Ala	Pro	Asp	His	Ile	Ser	Val	Lys	Gln	Cys	
305					310					315					320	
CTG	CTG	GCC	ATC	CTA	ATC	TTG	GCG	CTG	GTG	GCC	ACT	ATC	TTC	TTC	GTG	1008
Leu	Leu	Ala	Ile	Leu	Ile	Leu	Ala	Leu	Val	Ala	Thr	Ile	Phe	Phe	Val	
				325					330					335		
TGC	ACT	GTG	GTG	CTG	GCG	GTC	CGC	CTC	TCC	CGC	AAG	GGC	CAC	ATG	TAC	1056
Cys	Thr	Val	Val	Leu	Ala	Val	Arg	Leu	Ser	Arg	Lys	Gly	His	Met	Tyr	
				340				345					350			
CCC	GTG	CGT	AAT	TAC	TCC	CCC	ACC	GAG	ATG	GTC	TGC	ATC	TCA	TCC	CTG	1104
Pro	Val	Arg	Asn	Tyr	Ser	Pro	Thr	Glu	Met	Val	Cys	Ile	Ser	Ser	Leu	
		355					360					365				
TTG	CCT	GAT	GGG	GGT	GAG	GGG	CCC	TCT	GCC	ACA	GCC	AAT	GGG	GGC	CTG	1152
Leu	Pro	Asp	Gly	Gly	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Asn	Gly	Gly	Leu	
	370					375					380					
TCC	AAG	GCC	AAG	AGC	CCG	GGC	CTG	ACG	CCA	GAG	CCC	AGG	GAG	GAC	CGT	1200
Ser	Lys	Ala	Lys	Ser	Pro	Gly	Leu	Thr	Pro	Glu	Pro	Arg	Glu	Asp	Arg	
385					390					395					400	
GAG	GGG	GAT	GAC	CTC	ACC	CTG	CAC	AGC	TTC	CTC	CCT	TAG				1239
Glu	Gly	Asp	Asp	Leu	Thr	Leu	His	Ser	Phe	Leu	Pro					
				405					410							

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Pro	Leu	Gln	Leu	Leu	Leu	Leu	Ile	Leu	Leu	Gly	Pro	Gly	Asn	
1				5				10					15		
Ser	Leu	Gln	Leu	Trp	Asp	Thr	Trp	Ala	Asp	Glu	Ala	Glu	Lys	Ala	Leu
		20					25						30		
Gly	Pro	Leu	Leu	Ala	Arg	Asp	Arg	Arg	Gln	Ala	Thr	Glu	Tyr	Glu	Tyr
		35				40						45			
Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro	Glu	Met	Leu	Arg
	50					55					60				
Asn	Ser	Thr	Asp	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gly	Thr	Pro	Glu	Ser
65					70					75				80	
Thr	Thr	Val	Glu	Pro	Ala	Ala	Arg	Arg	Ser	Thr	Gly	Leu	Asp	Ala	Gly
				85					90					95	
Gly	Ala	Val	Thr	Glu	Leu	Thr	Thr	Glu	Leu	Ala	Asn	Met	Gly	Asn	Leu
		100						105					110		
Ser	Thr	Asp	Ser	Ala	Ala	Met	Glu	Ile	Gln	Thr	Thr	Gln	Pro	Ala	Ala
		115					120					125			

Thr	Glu	Ala	Gln	Thr	Thr	Gln	Pro	Val	Pro	Thr	Glu	Ala	Gln	Thr	Thr	
130						135					140					
Pro	Leu	Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Arg	Leu	Thr	Ala	Thr	Glu	
145					150					155					160	
Ala	Gln	Thr	Thr	Pro	Leu	Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Pro	Pro	
				165					170					175		
Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Gln	Pro	Thr	Gly	Leu	Glu	Ala	Gln	
			180					185					190			
Thr	Thr	Ala	Pro	Ala	Ala	Met	Glu	Ala	Gln	Thr	Thr	Ala	Pro	Ala	Ala	
		195					200					205				
Met	Glu	Ala	Gln	Thr	Thr	Pro	Pro	Ala	Ala	Met	Glu	Ala	Gln	Thr	Thr	
210						215					220					
Gln	Thr	Thr	Ala	Met	Glu	Ala	Gln	Thr	Thr	Ala	Pro	Glu	Ala	Thr	Glu	
225					230					235					240	
Ala	Gln	Thr	Thr	Gln	Pro	Thr	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Pro	Leu	
				245					250					255		
Ala	Ala	Met	Glu	Ala	Leu	Ser	Thr	Glu	Pro	Ser	Ala	Thr	Glu	Ala	Leu	
			260					265					270			
Ser	Met	Glu	Pro	Thr	Thr	Lys	Arg	Gly	Leu	Phe	Ile	Pro	Phe	Ser	Val	
		275					280					285				
Ser	Ser	Val	Thr	His	Lys	Gly	Ile	Pro	Met	Ala	Ala	Ser	Asn	Leu	Ser	
		290				295					300					
Val	Asn	Tyr	Pro	Val	Gly	Ala	Pro	Asp	His	Ile	Ser	Val	Lys	Gln	Cys	
305					310					315					320	
Leu	Leu	Ala	Ile	Leu	Ile	Leu	Ala	Leu	Val	Ala	Thr	Ile	Phe	Phe	Val	
				325					330					335		
Cys	Thr	Val	Val	Leu	Ala	Val	Arg	Leu	Ser	Arg	Lys	Gly	His	Met	Tyr	
			340					345					350			
Pro	Val	Arg	Asn	Tyr	Ser	Pro	Thr	Glu	Met	Val	Cys	Ile	Ser	Ser	Leu	
		355					360					365				
Leu	Pro	Asp	Gly	Gly	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Asn	Gly	Gly	Leu	
		370				375					380					
Ser	Lys	Ala	Lys	Ser	Pro	Gly	Leu	Thr	Pro	Glu	Pro	Arg	Glu	Asp	Arg	
385					390					395					400	
Glu	Gly	Asp	Asp	Leu	Thr	Leu	His	Ser	Phe	Leu	Pro					
				405					410							

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: pacesol

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGAGCTGA	GGCCCTGGTT	GCTATGGGTG	GTAGCAGCAA	CAGGAACCTT	GGTCCTGCTA	60
GCAGCTGATG	CTCAGGGCCA	GAAGGTCTTC	ACCAACACGT	GGGCTGTGCG	CATCCCTGGA	120
GGCCCAGCGG	TGGCCAACAG	TGTGGCACGG	AAGCATGGGT	TCCTCAACCT	GGGCCAGATC	180
TTCGGGGACT	ATTACCACTT	CTGGCATCGA	GGAGTGACGA	AGCGGTCCCT	GTCGCCTCAC	240
CGCCCGCGGC	ACAGCCGGCT	GCAGAGGGAG	CCTCAAGTAC	AGTGGCTGGA	ACAGCAGGTG	300
GCAAAGCGAC	GGACTAAACG	GGACGTGTAC	CAGGAGCCCA	CAGACCCCAA	GTTTCCTCAG	360
CAGTGGTACC	TGTCTGGTGT	CACTCAGCGG	GACCTGAATG	TGAAGGCGGC	CTGGGCGCAG	420
GGCTACACAG	GGCACGGCAT	TGTGGTCTCC	ATTCTGGACG	ATGGCATCGA	GAAGAACCAC	480
CCGGAATTGG	CAGGCAATTA	TGATCCTGGG	GCCAGTTTGT	ATGTCAATGA	CCAGGACCCCT	540
GACCCCCAGC	CTCGGTACAC	ACAGATGAAT	GACAACAGGC	ACGGCACACG	GTGTGCGGGG	600
GAAGTGGCTG	CGGTGGCCAA	CAACGGTGTC	TGTGGTGTAG	GTGTGGCCTA	CAACGCCCGC	660
ATTGGAGGGG	TGCGCATGCT	GGATGGCGAG	GTGACAGATG	CAGTGGAGGC	ACGCTCGCTG	720
GGCCTGAACC	CCAACCACAT	CCACATCTAC	AGTGCCAGCT	GGGGCCCCGA	GGATGACGGC	780
AAGACAGTGG	ATGGGCCAGC	CCGCCTCGCC	GAGGAGGCCT	TCTTCCGTGG	GGTTAGCCAG	840
GGCCGAGGGG	GGCTGGGCTC	CATCTTTGTC	TGGGCCTCGG	GGAACGGGGG	CCGGGAACAT	900
GACAGCTGCA	ACTGCGACGG	CTACACCAAC	AGTATCTACA	CGCTGTCCAT	CAGCAGCGCC	960
ACGCAGTTTG	GCAACGTGCC	GTGGTACAGC	GAGGCCTGCT	CGTCCACACT	GGCCACGACC	1020
TACAGCAGTG	GCAACCAGAA	TGAGAAGCAG	ATCGTGACGA	CTGACTTGCG	GCAGAAGTGC	1080
ACGGAGTCTC	ACACGGGCAC	CTCAGCCTCT	GCCCCCTTAG	CAGCCGGCAT	CATTGCTCTC	1140
ACCCTGGAGG	CCAATAAGAA	CCTCACATGG	CGGGACATGC	AACACCTGGT	GGTACAGACC	1200
TCGAAGCCAG	CCCACCTCAA	TGCCAACGAC	TGGGCCACCA	ATGGTGTGGG	CCGGAAAGTG	1260
AGCCACTCAT	ATGGCTACGG	GCTTTTGGAC	GCAGGCGCCA	TGGTGGCCCT	GGCCCAGAAT	1320
TGGACCACAG	TGGCCCCCCA	GCGGAAGTGC	ATCATCGACA	TCCTCACC GA	GCCCCAAGAC	1380
ATCGGGAAAC	GGCTCGAGGT	GCGGAAGACC	GTGACCGCGT	GCCTGGGCGA	GCCCCAACCAC	1440
ATCACTCGGC	TGGAGCACGC	TCAGGCGCGG	CTCACCCTGT	CCTATAATCG	CCGTGGCGAC	1500
CTGGCCATCC	ACCTGGTCAG	CCCCATGGGC	ACCCGCTCCA	CCCTGCTGGC	AGCCAGGCCA	1560
CATGACTACT	CCGCAGATGG	GTTTAATGAC	TGGGCCTTCA	TGACAACTCA	TTCCTGGGAT	1620
GAGGATCCCT	CTGGCGAGTG	GGTCCTAGAG	ATTGAAAACA	CCAGCGAAGC	CAACAACATAT	1680
GGGACGCTGA	CCAAGTTTAC	CCTCGTACTC	TATGGACCGG	CCCCTGAGGG	GCTGCCCCGTA	1740
CCTCCAGAAA	GCAGTGGCTG	CAAGACCCTC	ACGTCCAGTC	AGGCCTGTGT	GGTGTGCGAG	1800
GAAGGCTTCT	CCCTGCACCA	GAAGAGCTGT	GTCCAGCACT	GCCCTCCAGG	CTTCGCCCCC	1860

CAAGTCCTCG ATACGCACTA TAGCACCAG AATGACGTGG AGACCATCCG GGCCAGCGTC	1920
TGCGCCCCCT GCCACGCCTC ATGTGCCACA TGCCAGGGGC CGGCCCTGAC AGACTGCCTC	1980
AGCTGCCCCA GCCACGCCTC CTTGGACCCT GTGGAGCAGA CTTGCTCCCG GCAAAGCCAG	2040
AGCAGCCGAG AGTCCCCGCC ACAGCAGCAG CCACCTCGGC TGCCCCCGGA GGTGGAGGCG	2100
GGGCAACGGC TGCGGGCAGG GCTGCTGCCC TCACACCTGC CTGAGTGATG A	2151

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 (B) CLONE: sPSL.Fc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCCTCTGC AACTCCTCCT GTTGCTGATC CTACTGGGCC CTGGCAACAG CTTGCAGCTG	60
TGGGACACCT GGGCAGATGA AGCCGAGAAA GCCTTGGGTC CCCTGCTTGC CCGGGACCGG	120
AGACAGGCCA CCGAATATGA GTACCTAGAT TATGATTTC TGCCAGAAAC GGAGCCTCCA	180
GAAATGCTGA GGAACAGCAC TGACACCACT CCTCTGACTG GGCCTGGAAC CCCTGAGTCT	240
ACCACTGTGG AGCCTGCTGC AAGGCGTTCT ACTGGCCTGG ATGCAGGAGG GGCAGTCACA	300
GAGCTGACCA CGGAGCTGGC CAACATGGGG AACCTGTCCA CGGATTTCAGC AGCTATGGAG	360
ATACAGACCA CTCAACCAGC AGCCACGGAG GCACAGACCA CTCCACTGGC AGCCACAGAG	420
GCACAGACAA CTCGACTGAC GGCCACGGAG GCACAGACCA CTCCACTGGC AGCCACAGAG	480
GCACAGACCA CTCCACCAGC AGCCACGGAA GCACAGACCA CTCAACCCAC AGGCCTGGAG	540
GCACAGACCA CTGCACCAGC AGCCATGGAG GCACAGACCA CTGCACCAGC AGCCATGGAA	600
GCACAGACCA CTCCACCAGC AGCCATGGAG GCACAGACCA CTCAAACCAC AGCCATGGAG	660
GCACAGACCA CTGCACCAGA AGCCACGGAG GCACAGACCA CTCAACCCAC AGCCACGGAG	720
GCACAGACCA CTCCACTGGC AGCCATGGAG GCCCTGTCCA CAGAACCAG TGCCACAGAG	780
GCCCTGTCCA TGGAACTTAC TACCAAAAGA GGTCTGTTCA TACCCTTTTC TGTGTCCTCT	840
GTTACTCACA AGGGCATTCC CATGGCAGCC AGCAATTTGT CCGTCCTGCG GCCGCAGTCT	900
AGAGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA	960
GTCTTCCTCT TCCCCCAAAA ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC	1020
ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG	1080
GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG	1140

TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC 1200
 AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GTCCCATCG AGAAAACCAT CTCCAAAGCC 1260
 AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC CATCCCGGGA GGAGATGACC 1320
 AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG 1380
 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC 1440
 TCCGACGGCT CCTTCTTCCT CTATAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG 1500
 GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG 1560
 AGCCTCTCCC TGTCCCCGGG TAAATAG 1587

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTCGTCG ACTCTAGAG 19

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCTAGAGTC GACGG 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGCATACGC TCTAGAGCAT GGATCCCCTG GGTGCAGCCA AGC 43

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGAATTCT CAGGTGAACC AAGCCGC

27

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGTATCTGT CCAGGGCTTC CAGGT

25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACTACCCAG TGGGAGCACC AGACCACATC TCTGTGAAGC AGTGCTAG

48

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTCTAGCA CTGCTTCACA GAGATGTGGT CTGGTGCTCC CACTGGGTAG TT

52

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACTACCCAG TGGGAGCACC AGACCACATC TCTGTGAAGC AGTAG

45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATTCTACTG CTTACAGAG ATGTGGTCTG GTGCTCCAC TGGGTAGTT

49

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTAGACCCGG GATGGCATCC ATGACAGGAG GACAACAAAT GGTAGGCCGT AG

52

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AATTCTACGG CCTACCCATT TGTGTCTCTC CTGTCATGGA TGCCATCCCG GGT

53

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCGGCCGC AGT

13

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTAGACTGCG GCCGCAG

17

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGGTCCAA CTGCAGGTCG ACTCTAGAGG GCACTTCTTC TGGGCCCACG

60

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TATTATCTGT GCGGCCGCCC TCCAGAACCC ATGGCTGCTG GTTGCACTGG

60

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
TATTATCTGT GCGGCCGCGC AGCAGGCTCC ACAGTGGTAG 40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
TATTATCTGT GCGGCCGCGG AGGCTCCGTT TCTGGCAG 38

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CGGAGACAGG CCACCGAATT CCTGCCAGAA ACG 33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
CCTCCAGAAA TGCTGAGGCA CAGCACTGAC ACCACTCCTC 40

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTGGCCA ACATGGGGCA ACTGTCCACG GATTCAGCAG

40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AATTCGAGTT CCTAGATTTT G

11

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AATTCAAAAT CTAGGAACTC G

11

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AATTCGAGTA CCTAGATTAT GATTTCCTGC CAGAAACTGA GCCTCCGC

48

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCCGCGGAG GCTCAGTTTC TGGCAGGAAA TCATAATCTA GGTACTCG

48

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AATTCGAGTT CCTAGATTAT GATTCCTGC CAGAACTGA GCCTCCGC

48

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCCGCGGAG GCTCAGTTTC TGGCAGGAAA TCATAATCTA GGAACCTG

48

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AATTCGAGTT CCTAGATTTC GATTCCTGC CAGAACTGA GCCTCCGC

48

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGCCGCGGAG GCTCAGTTTC TGGCAGGAAA TCGAAATCTA GGAACCTG

48

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

ATGCCTCTGC AACTCCTCCT GTTGCTGATC CTACTGGGCC CTGGCAACAG CTTGCAGCTG      60
TGGGACACCT GGGCAGATGA AGCCGAGAAA GCCTTGGGTC CCCTGCTTGC CCGGGACCGG      120
AGACAGGCCA CCGAATATGA GTACCTAGAT TATGATTTC T GCCAGAAAC GGAGCCTCCA      180
GAAATGCTGA GGAACAGCAC TGACACCACT CCTCTGACTG GGCCTGGAAC CCCTGAGTCT      240
ACCACTGTGG AGCCTGCTGC GCGGCCGCAC ACATGCCCAC CGTGCCCAGC ACCTGAAGCC      300
CTGGGGGCAC CGTCAGTCTT CCTCTTCCCC CAAAACCCA AGGACACCCT CATGATCTCC      360
CGGACCCCTG AGGTCACATG CGTGGTGGTG GACGTGAGCC ACGAAGACCC TGAGGTCAAG      420
TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC GCGGGAGGAG      480
CAGTACAACA GCACGTACCG TGTGGTCAGC GTCCTCACCG TCCTGCACCA GGACTGGCTG      540
AATGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGCCC TCCCAGTCCC CATCGAGAAA      600
ACCATCTCCA AAGCCAAAGG GCAGCCCCGA GAACCACAGG TGACACCCT GCCCCATCC      660
CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC      720
AGCGACATCG CCGTGGAGTG GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG      780
CCTCCCGTGC TGGACTCCGA CGGCTCCTTC TTCCTCTATA GCAAGCTCAC CGTGGACAAG      840
AGCAGGTGGC AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC      900
CACTACACGC AGAAGAGCCT CTCCTGTCC CCGGTAAAT GA                          942

```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1           5           10           15

Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu

```


(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
ATGCTCTGTC AACTCCTCCT GTTGCTGATC CTA CTGGGCC CTGGCAACAG CTTGCAGCTG      60
TGGGACACCT GGGCAGATGA AGCCGAGAAA GCCTTGGGTC CCCTGCTTGC CCGGGACCGG      120
AGACAGGCCA CCGAATATGA GTACCTAGAT TATGATTTCC TGCCAGAAAC GGAGCCTCCA      180
GAAATGCTGA GGAACAGCAC TGACACCACT CCTCTGACTG GGCCTGGAAC CCCTGAGTCT      240
ACCACTGTGG AGCCTGCTGC GCGGCCGCTG TGTGCCAACC TAGTACCGGT GCCCATCACC      300
AACGCCACCC TGGACCAGAT CACTGGCAAG TGGTTTATA TCGCATCGGC CTTTCGAAAC      360
GAGGAGTACA ATAAGTCGGT TCAGGAGATC CAAGCAACCT TCTTTTACTT CACCCCCAAC      420
AAGACAGAGG ACACGATCTT TCTCAGAGAG TACCAGACCC GACAGGACCA GTGCATCTAT      480
AACACCACCT ACCTGAATGT CCAGCGGGAA AATGGGACCA TCTCCAGATA CGTGGGAGGC      540
CAAGAGCATT TCGCTCACTT GCTGATCCTC AGGGACACCA AGACCTACAT GCTTGCTTTT      600
GACGTGAACG ATGAGAAGAA CTGGGGGCTG TCTGTCTATG CTGACAAGCC AGAGACGACC      660
AAGGAGCAAC TGGGAGAGTT CTACGAAGCT CTCGACTGCT TGCGCATTCC CAAGTCAGAT      720
GTCGTGTACA CCGATTGGAA AAAGGATAAG TGTGAGCCAC TGGAGAAGCA GCACGAGAAG      780
GAGAGGAAAC AGGAGGAGGG GGAATCCTAG                                         810
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1           5           10           15
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
20           25           30
Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
35           40           45
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
50           55           60
Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65           70           75           80
Thr Thr Val Glu Pro Ala Ala Arg Pro Leu Cys Ala Asn Leu Val Pro
85           90           95
```

Val Pro Ile Thr Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe
100 105 110

Tyr Ile Ala Ser Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln
115 120 125

Glu Ile Gln Ala Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp
130 135 140

Thr Ile Phe Leu Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr
145 150 155 160

Asn Thr Thr Tyr Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg
165 170 175

Tyr Val Gly Gly Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp
180 185 190

Thr Lys Thr Tyr Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp
195 200 205

Gly Leu Ser Val Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu
210 215 220

Gly Glu Phe Tyr Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp
225 230 235 240

Val Val Tyr Thr Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys
245 250 255

Gln His Glu Lys Glu Arg Lys Gln Glu Glu Gly Glu Ser
260 265

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGTGGCCG GGACCCGCTG TCTTCTAGCG TTGCTGCTTC CCCAGGTCCT CCTGGGCGGC 60

GCGGCTGGCC TCGTTCCGGA GCTGGGCCGC AGGAAGTTTCG CGGCGGCGTC GTCGGGCCGC 120

CCCTCATCCC AGCCCTCTGA CGAGGTCCTG AGCGAGTTTCG AGTTGCGGCT GCTCAGCATG 180

TTCGGCCTGA AACAGAGACC CACCCCAGC AGGGACGCCG TGGTGCCCCC CTACATGCTA 240

GACCTGTATC GCAGGCACTC AGGTCAGCCG GGCTCACCCG CCCCAGACCA CCGGTTGGAG 300

AGGGCAGCCA GCCGAGCCAA CACTGTGCGC AGCTTCCACC ATGAAGAATC TTTGGAAGAA 360

CTACCAGAAA CGAGTGGGAA AACAACCCGG AGATTCTTCT TTAATTTAAG TTCTATCCCC 420

ACGGAGGAGT TTATCACCTC AGCAGAGCTT CAGGTTTTTC GAGAACAGAT GCAAGATGCT 480

TTAGGAAACA ATAGCAGTTT CCATCACCGA ATTAATATTT ATGAAATCAT AAAACCTGCA 540
 ACAGCCAACT CGAAATTCCC CGTGACCAGA CTTTGGGACA CCAGGTTGGT GAATCAGAAT 600
 GCAAGCAGGT GGGAAAGTTT TGATGTCACC CCCGCTGTGA TGCGGTGGAC TGCACAGGGA 660
 CACGCCAACC ATGGATTTCG GGTGGAAGTG GCCCACTTGG AGGAGAAACA AGGTGTCTCC 720
 AAGAGACATG TTAGGATAAG CAGGTCTTTG CACCAAGATG AACACAGCTG GTCACAGATA 780
 AGGCCATTGC TAGTAAC TTT TGGCCATGAT GGAAAAGGGC ATCCTCTCCA CAAAAGAGAA 840
 AAACGTCAGG CCACCGAATA TGAGTACCTA GATTATGATT TCCTGCCAGA AACGGAGCCT 900
 CCAGAAATGC TGAGGAACAG CACTGACACC ACTCCTCTGA CTGGGCCTGG AACCCTGAG 960
 TCTACCACTG TGGAGCCTGC TGCAAGGCGG AAACGCCTTA AGTCCAGCTG TAAGAGACAC 1020
 CCTTTGTACG TGGACTTCAG TGACGTGGGG TGAATGACT GGATTGTGGC TCCCCCGGGG 1080
 TATCACGCCT TTTACTGCCA CGGAGAATGC CCTTTTCCTC TGGCTGATCA TCTGAACTCC 1140
 ACTAATCATG CCATTGTTCA GACGTTGGTC AACTCTGTTA ACTCTAAGAT TCCTAAGGCA 1200
 TGCTGTGTCC CGACAGAACT CAGTGCTATC TCGATGCTGT ACCTTGACGA GAATGAAAAG 1260
 GTTGTATTAA AGAACTATCA GGACATGGTT GTGGAGGGTT GTGGGTGTCTG CTAG 1314

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Val	Ala	Gly	Thr	Arg	Cys	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	Val
1				5					10					15	
Leu	Leu	Gly	Gly	Ala	Ala	Gly	Leu	Val	Pro	Glu	Leu	Gly	Arg	Arg	Lys
		20					25					30			
Phe	Ala	Ala	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Ser	Gln	Pro	Ser	Asp	Glu
		35					40					45			
Val	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	Phe	Gly	Leu	Lys
		50				55					60				
Gln	Arg	Pro	Thr	Pro	Ser	Arg	Asp	Ala	Val	Val	Pro	Pro	Tyr	Met	Leu
65				70					75					80	
Asp	Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp
				85				90					95		
His	Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe
		100					105					110			
His	His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr
		115				120						125			

Thr	Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	130	135	140
Ile	Thr	Ser	Ala	Glu	Leu	Gln	Val	Phe	Arg	Glu	Gln	Met	Gln	Asp	Ala	145	150	155
Leu	Gly	Asn	Asn	Ser	Ser	Phe	His	His	Arg	Ile	Asn	Ile	Tyr	Glu	Ile	165	170	175
Ile	Lys	Pro	Ala	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	180	185	190
Asp	Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Ser	Phe	Asp	195	200	205
Val	Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	210	215	220
Gly	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	225	230	235
Lys	Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser	245	250	255
Trp	Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys	260	265	270
Gly	His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Thr	Glu	Tyr	Glu	275	280	285
Tyr	Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro	Glu	Met	Leu	290	295	300
Arg	Asn	Ser	Thr	Asp	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gly	Thr	Pro	Glu	305	310	315
Ser	Thr	Thr	Val	Glu	Pro	Ala	Ala	Arg	Arg	Lys	Arg	Leu	Lys	Ser	Ser	325	330	335
Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	340	345	350
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly	355	360	365
Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	370	375	380
Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	385	390	395
Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	405	410	415
Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	Glu	420	425	430
Gly	Cys	Gly	Cys	Arg												435		

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
ATGCCTCTGC AACTCCTCCT GTTGCTGATC CTACTGGGCC CTGGCAACAG CTTGCAGCTG      60
TGGGACACCT GGGCAGATGA AGCCGAGAAA GCCTTGGGTC CCCTGCTTGC CCGGGACCGG      120
AGACAGGCCA CCGAATATGA GTACCTAGAT TATGATTTCC TGCCAGAAAC GGAGCCTCCA      180
GAAATGCTGA GGAACAGCAC TGACACCACT CCTCTGACTG GGCCTGGAAC CCCTGAGTCT      240
ACCACTGTGG AGCCTGCTGC GCGGCCGCCA CCTGGCCCCC CTCGAGTTTC CCCAGACCTT      300
CGGGCCGAGC TGGACAGCAC CGTGCTCCTG ACCCGCTCTC TCCTGGCGGA CACGCGGCAG      360
CTGGCTGCAC AGCTGAGGGA CAAATTCCCA GCTGACGGGG ACCACAACCT GGATTCCCTG      420
CCCACCCTGG CCATGAGTGC GGGGGCACTG GGAGCTCTAC AGCTCCCAGG TGTGCTGACA      480
AGGCTGCGAG CGGACCTACT GTCCTACCTG CGGCACGTGC AGTGGCTGCG CCGGGCAGGT      540
GGCTCTTCCC TGAAGACCCT GGAGCCCGAG CTGGGCACCC TGCAGGCCCG ACTGGACCGG      600
CTGCTGCGCC GGCTGCAGCT CCTGATGTCC CGCCTGGCCC TGCCCCAGCC ACCCCCGGAC      660
CCGCCGGCGC CCCCCTGGC GCCCCCTCC TCAGCCTGGG GGGGCATCAG GGCCGCCAC      720
GCCATCCTGG GGGGGCTGCA CCTGACACTT GACTGGGCCG TGAGGGGACT GCTGCTGCTG      780
AAGACTCGGC TGTGA                                                    795
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1           5           10           15
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
20           25           30
Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
35           40           45
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
50           55           60
Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
```


